In the Specification:

Please replace the paragraph on page 30, line 29 to page 31, line 9 with the following:

The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. U.S.A. 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. U.S.A. 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al., 1990, J. Mol. Biol. 215:403-0. BLAST nucleotide searches can be performed with the NBLAST nucleotide program parameters set, e.g., for score=100, wordlength=12 to obtain nucleotide sequences homologous to a donor or target nucleic acid. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-BLAST can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., of XBLAST and NBLAST) can be used (see, e.g., www.ncbi.nlm.nih.gov). Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) CABIOS 4:11-17. Such an algorithm is incorporated in the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package.

Please replace the paragraph on page 47, lines 3-16 with the following:

The pGPG plasmid is a derivative of the R6K plasmid. The plasmid R6K can be transferred between strains by conjugation (Macrina et al., 1974, J. Bacteriol. 120(3):1387-1400). A significant number of derivatives of R6K have been created, among which are plasmids defective for conjugation (Nunez et al., 1997, Mol. Microbiol. 24:1157-68), replication (Kolter, 1981, Plasmid 5(1):2-9), or for both conjugation and replication (Metcalf et al., 1994, Gene 138:1-7). The plasmids can be rescued by providing the conjugation and/or replication functions in trans. An R6K derivative where replication and conjugation functions are provided in trans is desirable as a donor vector. Once such a derivative is transferred to a target strain which lacks the replication and conjugation functions, the vector DNA exists transiently pending dilution

following bacterial growth. The vector DNA is available for recombination, but (in the absence of recombination) will rapidly be lost and will not replicate or participate in subsequent conjugational events. One such plasmid, pGP704 (salmonella.org.vectors/pgp704/), was used as starting point for the creation of the pGPG series of vectors suitable for DGA.

Please replace the paragraph on page 52, line 31 to page 53, line 2 with the following:

The galactose resistance selection requires a strain with a defect in both the galactose kinase gene (galK) and a defect in the galactose epimerase gene (galE). In such a strain, expression of GalK from the Gal-Spec cassette (described in Section 6.2.3) is lethal in the presence of galactose and selection for growth in the presence of galactose is a selection for loss of the cassette. The bacterial strain OTG2 (also known as KS272; Dr. Stanley Maloy, salmonella.life.uiuc.edu/strainfinder- .html) has defective galK and galE genes.